

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 05:39:13 ; Search time 2503.5 Seconds
(without alignments)
11433.036 Million cell updates/sec

Title: US-09-811-093-42

Perfect score: 1735

Sequence: 1 agcgatacaatttcac.....taattggaagcttgtagt 1735

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htgo_hum.*
- 31: em.htgo_inv.*
- 32: em.htgo_rod.*
- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	139.8	8.1	104992	2	AC005504	AC005504 Plasmodiu
2	139.8	8.1	169546	2	AC004157	AC004157 Plasmodiu
3	139.6	8.0	144493	9	AP001547	AP001547 Homo sapi
4	135.4	7.8	67970	3	PFMAL1P3	AL031746 Plasmodiu
5	135	7.8	86827	3	PFMAL3P5	AL034556 Plasmodiu
6	134.4	7.7	173915	9	AP001254	AP001254 Homo sapi
7	134.4	7.7	340000	9	AP001678	AP001678 Homo sapi
8	134.2	7.7	172805	9	AC066608	AC066608 Homo sapi
9	133.8	7.7	172666	2	AC046181	AC046181 Homo sapi
10	133.6	7.7	176174	9	AC007483	AC007483 Homo sapi
11	133.4	7.7	326924	2	AC093082	AC093082 Homo sapi
12	132.2	7.6	104992	2	AC005504	AC005504 Plasmodiu
13	132.2	7.6	169546	2	AC004157	AC004157 Plasmodiu
14	132.2	7.6	188930	2	AC091742	AC091742 Homo sapi
15	132	7.6	12029	3	AE001422	AE001422 Plasmodiu
16	131.4	7.6	293431	2	PFMAL13P4	AL049181 Plasmodiu
17	130.8	7.5	137889	9	AC073269	AC073269 Homo sapi
18	130.8	7.5	175223	9	AC004617	AC004617 Homo sapi
19	130.8	7.5	326924	2	AC093082	AC093082 Homo sapi
20	130.6	7.5	14867	3	AE001398	AE001398 Plasmodiu
21	130.6	7.5	143331	9	AC091214	AC091214 Homo sapi
22	129.6	7.5	185691	2	AC021553	AC021553 Homo sapi
23	129.2	7.4	150724	9	AP000550	AP000550 Homo sapi
24	129.2	7.4	180884	9	AC008018	AC008018 Homo sapi
25	129	7.4	4601	3	DMU11584	U11584 Drosophilla
26	129	7.4	19517	3	DMU37541	U37541 Drosophilla
27	129	7.4	149733	2	AC087568	AC087568 Pan trogl
28	128.8	7.4	14867	3	AE001398	AE001398 Plasmodiu
29	128.6	7.4	28862	9	AC012398	AC012398 Homo sapi
30	128.6	7.4	156933	2	AC026839	AC026839 Homo sapi
31	128.2	7.4	4601	3	DMU11584	U11584 Drosophilla
32	128.2	7.4	19517	3	DMU37541	U37541 Drosophilla
33	127.6	7.4	196152	2	AC097976	AC097976 Homo sapi
34	126.6	7.3	106763	9	AP002091	AP002091 Homo sapi
35	126.6	7.3	318221	2	PFMAL13P3	AL049184 Plasmodiu
36	126.2	7.3	86827	3	PFMAL3P5	AL034556 Plasmodiu
37	125.2	7.2	106763	9	AP002091	AP002091 Homo sapi
38	125.2	7.2	187953	2	AC010948	AC010948 Homo sapi
39	125	7.2	108902	2	AC011430	AC011430 Homo sapi
40	124.8	7.2	106650	9	AC007708	AC007708 Homo sapi
41	124.8	7.2	205429	2	AC005506	AC005506 Plasmodiu
42	123.8	7.1	218078	2	AC068138	AC068138 Homo sapi
43	123.6	7.1	67970	3	PFMAL1P3	AL031746 Plasmodiu
44	123.6	7.1	173349	2	AL596253	AL596253 Homo sapi
45	123.4	7.1	122364	9	AC007324	AC007324 Homo sapi

ALIGNMENTS

RESULT 1
AC005504
LOCUS AC005504 104992 bp DNA HTG 01-APR-1999
DEFINITION Plasmodium falciparum chromosome 12, *** SEQUENCING IN PROGRESS
AC005504
AC005504
AC005504
AC005504.3 GI:4558584
VERSION HTG; HTGS-PHASE1.
KEYWORDS malaria parasite P. falciparum.
SOURCE Plasmodium falciparum
ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE 1 (bases 1 to 104992)
Hyman,R.W., Fung,E.L., Qin,F., Tamaki,T., Kurdi,O.B., Conway,A.B.
and Davis,R.W.
TITLE Plasmodium falciparum 3D7 chromosome 12
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 104992)
Hyman,R.W., Qin,F., Fung,E.L., Conway,A.B. and Davis,R.W.
AUTHORS Direct Submission
TITLE Direct Submission
JOURNAL Submitted (21-AUG-1998) Stanford DNA Sequencing and Technology

Qy	1199	tcgtattgaattctttttattcaaaaaaaccccaaaatttttaaaacctgtttgcgaatagac	1258
Db	27266	ATGTATGTTTATGTAATTAATAAATAATATGATGTTTATGTTATTAATAAATAATA	27207
Qy	1259	caatatagtttaacatcgctggtctattgttagataaaattgaaatttcttattttaa	1318
Db	27206	ATGTATGTTTATGTAATTAATAAATAATATGATGTTTATGTTATTAATAAATAATA	27147
Qy	1319	taaatatttgattttatttgatataatttgcatttagatacaaaaattaaatttaaata	1378
Db	27146	ATATATGTTTATGTAATTAATAAATAATATATATGTTTATGTTATTAATAAATAATA	27087
Qy	1379	ttattttatcttcaataaataacatttgcgttaatttttctatttttagaccatttcttca	1438
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Qy	1439	tttttataaacattttaaatacaaaatgaatgtagacacacataattatttttatcca	1498
Db	27026	TTTATATATATGTAATTAATAAATAATATATATTAATATATGTAATTAATAAATAATA	26967
Qy	1499	aagaaaaaatgcgtataaaatgatggctcttcttacccttcattgataaattatgaaaaa	1558
Db	26966	TTTGTATATATATATTAATAAATAATATATATATATATATATATATATATATATATA	26907
Qy	1559	taaaataaaatttaattatata 1580	
Db	26906	TAATATATATTTTATTTATATATA 26885	

RESULT 4

PFMALP3 67970 bp DNA INV 15-DEC-1999

LOCUS Plasmodium falciparum MALLP3, complete sequence.

DEFINITION AL031746

ACCESSION AL031746.9 GI:6594243

VERSION HTG.

KEYWORDS malaria parasite P. falciparum.

SOURCE Plasmodium falciparum

ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

REFERENCE 1 (bases 1 to 67970)

AUTHORS Bowman,S., Churcher,C., Harris,B., Harris,D., Lawson,D., Quail,M. and Barrett,B.

TITLE Direct Submision

JOURNAL Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, UK

COMMENT On Dec 16, 1999 this sequence version replaced gi:5763807. For more information about this sequence or the Malaria Project, see <http://www.sanger.ac.uk/Projects/P.falciparum>. IMPORTANT: This sequence is unfinished and does not necessarily represent the correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc.

FEATURES

source Location/Qualifiers

1..67970

/organism="Plasmodium falciparum"

/strain="3D7"

/db_xref="taxon:5833"

/chromosome="1"

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/gene="MALLP3.01"

/note="MALLP3.01, conserved hypothetical protein, len: 412 aa, similarity: upf0006:family eg to YBL055C/YBL0512/YBL0511, YBF5_YEAST (418 aa), fasta scores: Opt: 316, E(): 1.1e-12, (33.2% identity in 271 aa overlap)"

/codon_start=1

/product="conserved hypothetical protein, upf0006 family"

Hennig,S., Riesselmann,L., Dagand,E., Wehrmaeyer,S., Borzym,K.,
Gardiner,K., Nizetic,D., Francis,F., Lehrach,H., Reinhardt,R. and
Yaspo,M.L.

TITLE JOURNAL

Submitted (10-APR-2000) to the DBJ/EMBL/GenBank databases. The
Chromosome 21 Mapping and Sequencing Consortium: * RIKEN Genomic
Sciences Center, Human Genome Research Group * Institute of
Molecular Biotechnology, Genome Analysis * Keio University School
of Medicine, Dept. of Molecular Biology * GBF, Dept. of Genome
Analysis * Max-Planck Institute for Molecular Genetics (addresses
see below)

COMMENT

On May 30, 2000 this sequence version replaced gi:7717275.
The chromosome 21 mapping and sequencing consortium consisting of
* RIKEN Genomic Sciences Center, Human Genome Research Group, *
Sagami-hara 228-8555, Japan,
* e.mail: hattori@gsc.riken.go.jp
* URL: http://hgp.gsc.riken.go.jp/
and

* Institute of Molecular Biotechnology, Genome Analysis, *
Beutenbergstrasse 11, D-07745 Jena, Germany,
* e.mail: gscj-submit@genome.imb-jena.de
* URL: http://genome.imb-jena.de/
and

* Keio University School of Medicine, Molecular Biology, * Tokyo
160-8562, Japan,
* e.mail: nshimizuedmb-med.keio.ac.jp
* URL: http://www.dmb.med.keio.ac.jp/
and

* GBF, Dept. of Genome Analysis,
* Mascheroder Weg 1, D-38124 Braunschweig, Germany, * e.mail:
info.genome@gbf.de
* URL: http://genome.gbf.de/
and

* Max-Planck Institute for Molecular Genetics,
* Ihnestrasse 73, D-14195 Berlin, Germany,
* e.mail: info-chr21@molgen.mpg.de
* URL: http://chr21.rz-berlin.mpg.de/
AL163223: Submitted (10-APR-2000).
Location/Qualifiers
1. 340000
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="21"
<1. 14692
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/db_xref="taxon:9606"
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<1. 121279
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/organism="Homo sapiens"
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/chromosome="21"
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/clone="R732H1, 5' partial"
/clone_lib="RPCI-11 BAC library"
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1731. 1890
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1891. 2300
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2301. 2431
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FEATURES source

source

source

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repeat_region

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/rpt_family="LTR/Retroviral"
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/note="AluSq"
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/note="AluSq"
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/rpt_type=DISPERSED
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/note="AluX"
/rpt_family="SINE/Alu"

[illegible]

[illegible]

FEATURES

Query Match 7.7%; Score 133.4; DB 2;
Best Local Similarity 46.4%; Pred. No. 1.6e-07;
Matches 540; Conservative 0; Mismatches 616; Indels 7; Gaps 3;

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134116. .143412
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151993. .164752
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Best Local Similarity 46.4%; Pred. No. 1.6e-07;
Matches 540; Conservative 0; Mismatches 616; Indels 7; Gaps 3
QY 435 tttttcacatcgtaaccaaatctaaagatcggtatataaaggaatcctcaaaaaa 494
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Db 292825 TTTTATAATTTATATAAAATTTAATAATTTATATAATTTATATAATTTAA 292766
QY 495 ttgtttgagttggagtagcacaatttcaacaaatcgcgtaaaaaataaacgacgtaga 554
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Db 292765 TTAATATATATTAGTTAAATATATATTAAATTTATATATTTAATTAATAATAATA 292706
QY 555 caaatctaaacgatcgjgcacaaagatttaaaaaatcgttttagtcaaatcttaacaa 614
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Db 292705 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 292646
QY 615 ttgtataaccaaattaaacgatagaattgaaataataaaatcggttagattggcgcatcca 674
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Db 292645 ATAATATATTATATAAAATATATATAATTAATTAATTAATTAATTAATTAATTA 292586
QY 675 aatttaaatgacaaatctaaacgatcggtataaccaaatcaacgatcgkacacaaatc 734
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QY 735 taaatgatcatgctaccaaatattatgatcatgttggcagggtgggtgcaggcaacatt 794
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QY 795 ttgtatatcttctattatgggtttgtagaatttttcatttcgaaatgttctctatacaa 854
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QY 855 tataaataataaattttccaaacttgcatttttcgaaagagcccttaataaattg 914
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Db 292406 TATATATTATAATATATAAATATATAATTAATTAATTAATTAATTAATTAATTA 292347
QY 915 aattcgcatataaattttccaaataaagtagactatgctctatccaaatatt 974
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QY 975 gattcccaatatagaaceaatctcaaatgaacaaacatttgaaattctcgatatagaa 1034
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Db 292291 TATATATAAATATATATTATTAATTAATTAATTAATTAATTAATTAATTAATTA 292232
QY 1035 aacatttactattttggaattgggacatatcccaagtttattccaaacgtaactttgaa 1094
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Db 292231 TTAATATATATGATATATATTATATAAATATATAATTAATTAATTAATTAATTA 292172
QY 1095 ggaaagtgttagagattacatcccatattttgtttttcatattgaaatttcattggaaa 1154
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Qy	1075	attccaaacgtaa-----ctttgaaggaaaagttagtgagatcatccatat	1126
Dd	85429	AATTAATATAAAAATAAACCATTTTATACTTAATTAATATATAAATAAATAAT	85370
Qy	1127	tgttttcataatgaattcattcggaataataaatgcacacaaaatgatgtgagatta	1186
Dd	85369	TAAATGTGTAATAAATAAATAAACAATTATTAAATAAATAATATATATAATTA	85310
Qy	1187	aaccaaaagtcttgttatgaattccttttataaaaaaaccaacaanaatttaaaact	1246
Dd	85309	TATATATCTCTAAATAATAATTTTTTAAATATTTTAAATAAATAATATTAAT	85250
Qy	1247	tttgcagaagaccaataatagttcaaaccatcggtctattgcagatacaaatgtga	1306
Dd	85249	ATTAAATTATGATATTTTAAATGGTTTAAATTTATATTTATTTATTTATTA	85191
Qy	1307	tgttatattaataaatatttggattatttbtgatatatttgcattagatacaaaa	1366
Dd	85190	TATTAATTAATAATTAATATATATATATTTAAATTAATTAATTAATTAATTA	85131
Qy	1367	aegattttaaatatttcttatctctaatacaacatttgttaattttctctattaga	1426
Dd	85130	AATTT-----AATTATGGTTTATTAATATATATATATTAATTAATTAATTA	85076
Qy	1427	ccattctcttatttctatacaaccttttaacaactaaatgatgtgacacacactaa	1486
Dd	85075	TTTATATATATATATATATTAATTAATATAATAAATTAATTAATATATATTA	85016
Qy	1487	tattttatccaagaataatgctataaaaatgggtctctcttataccctccatgat	1546
Dd	85015	TATTTATATATTAATTAATTAATATATTTTAAATTAATTAATTAATTAATTA	84956
Qy	1547	aattatgaaaaataaaaattcaattcataataatcatttcattcctaatcgtacaag	1606
Dd	84955	TTTATTTTATTTAATTAATTAATTAATTAATTAATATATAT-ATTTAATTA	84897
Qy	1607	agattactatatcaacaacttgcgtataaaaaggccaagaataaagcattatcgt	1666
Dd	84896	TTTAAATTAATATATATATATTAATTAATTAATTAATTAATTAATTAATTA	84837
Qy	1667	tgagccactttctctatctagagatagaaggtttaaaatcatgctctctaatgg	1725
Dd	84836	TTATTAATTTATTTATATATTAATTAATTAATTAATTTATTTATTTTAACTAA	84778
RESULT	14		
LOCUS	AC091742/c		
DEFINITION	Homo sapiens chromosome UNK clone RP11-1220K2, WORKING DRAFT SEQUENCE, 4 unordered pieces.	DNA	HTG 09-AUG-2001
ACCESSION	AC091742		
VERSION	AC091742.4	GI:15144365	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	The sequence of Homo sapiens clone		
JOURNAL	Unpublished		
AUTHORS	Waterston,R.H.		
REFERENCE	2 (bases 1 to 188930)		
TITLE	Direct Submission		
JOURNAL	Submitted (27-MAY-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis MO 63108, USA		
COMMENT	On Aug 9, 2001 this sequence version replaced gi:14339170.		

Search completed: April 2, 2002, 08:49:04
Job time: 11391 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 06:29:29 ; Search time 181.18 Seconds
(without alignments)
8209.843 Million cell updates/sec

Title: US-09-811-093-42
Perfect score: 1735
Sequence: 1 agcggatacaatttcacac.....taattggaagcttgtagt 1735

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues
Total number of hits satisfying chosen parameters: 1861242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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21: /SIDS2/gcgdata/geneseq/geneseq/NA2000.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	279	16.1	936	AAF58252	Oligonucleotide D1
C 2	279	16.1	936	AAF58254	Oligonucleotide D1
C 3	279	16.1	936	AAF58257	Oligonucleotide D1
C 4	279	16.1	936	AAF58259	Oligonucleotide D1
C 5	279	16.1	936	AAF58262	Oligonucleotide D2
C 6	279	16.1	936	AAF58255	Oligonucleotide D1
7	278.2	16.0	936	AAF58252	Oligonucleotide D1
8	278.2	16.0	936	AAF58254	Oligonucleotide D1
9	278.2	16.0	936	AAF58257	Oligonucleotide D1
10	278.2	16.0	936	AAF58259	Oligonucleotide D1
11	278.2	16.0	936	AAF58262	Oligonucleotide D2

C 12	278.2	16.0	938	22	AAF58255	Oligonucleotide D1
C 13	130	7.5	217	21	AAAG7340	Human UNK22-5' cDN
C 14	109.4	6.3	700	22	AAH93026	Human inflammatory
C 15	109	6.3	3244	20	AAH59168	Rat G protein coup
C 16	108.8	6.3	1272	19	AAV19124	Nucleotide sequenc
C 17	108	6.2	371	21	AAAF0054	Human ovarian carc
C 18	107.6	6.2	1410	22	AAAF91975	B thuringiensis 44
C 19	106.6	6.1	848	21	AAZ97334	Human prostate can
C 20	106.2	6.1	3908	22	AAAF13152	Escherichia coli T
C 21	105.2	6.1	724	21	AAZ97430	Human prostate can
C 22	105.2	6.1	740	21	AAZ97429	Human prostate can
C 23	105.2	6.1	817	21	AAZ97370	Human prostate can
C 24	105.2	6.1	1024	21	AAZ97209	Human prostate can
C 25	105.2	6.1	1024	21	AAZ97219	Human prostate can
C 26	104.8	6.0	771	21	AAZ97308	Human prostate can
C 27	104.8	6.0	809	21	AAZ97398	Human prostate can
C 28	104.8	6.0	815	21	AAZ97377	Human prostate can
C 29	104.8	6.0	822	21	AAZ97362	Human prostate can
C 30	104.8	6.0	823	21	AAZ97319	Human prostate can
C 31	104.8	6.0	827	21	AAZ97356	Human prostate can
C 32	104.8	6.0	1017	21	AAZ97187	Human prostate can
C 33	104.8	6.0	1024	21	AAZ97159	Human prostate can
C 34	104.8	6.0	1024	21	AAZ97217	Human prostate can
C 35	104.8	6.0	2016	22	AAAD3518	Mouse cell cycle c
C 36	104.8	6.0	2672	21	AAAH30885	Rat GFAT II coding
C 37	104.4	6.0	198	22	AAH83749	Human ovarian tumo
C 38	103.2	5.9	1024	21	AAZ97239	Human prostate can
C 39	102.8	5.9	775	21	AAZ97272	Human prostate can
C 40	102.6	5.9	1021	21	AAZ97242	Human prostate can
C 41	102	5.9	435	22	AAAF1792	Human breast cance
C 42	99.2	5.7	704	20	AAAF90804	Rat progression re
C 43	99.2	5.7	837	21	AAZ97338	Human prostate can
C 44	99.2	5.7	5990	22	AAAF80223	Nucleotide sequenc
C 45	99	5.7	779	21	AAZ97278	Human prostate can

ALIGNMENTS

RESULT 1
AAF58252/c
ID AAF58252 standard; DNA; 936 BP.
XX
AC AAF58252;
XX
DT 24-APR-2001 (first entry)
XX
DE Oligonucleotide D1835.
XX
KW Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression; ss.
XX
OS Synthetic.
XX
FN WO200107665-A2.
XX
PD 01-FEB-2001.
XX
PF 26-JUL-2000; 2000WO-US20476.
XX
PR 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
(CLIN-) CLINICAL MICRO SENSORS INC.
XX
UMek RM;
XX
WPI; 2001-159728/16.
XX
Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface

XX The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic


```
PN W0200107665-A2.
XX
XX
PD 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
PR 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
PA
XX Umek RM;
XX WPI; 2001-159728/16.
XX
XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 4 A; 144 C; 7 G; 5 T; 776 other;
SQ

Query Match 16.0%; Score 278.2; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 4.3e-29;
Matches 7; Conservative 613; Mismatches 161; Indels 0; Gaps 0;

Qy 823 aatttttcttcgaattgtctctacataataataataataatttttaccacttcgt 882
Db 2 www. ....
Qy 883 tatatttcgaagacccttaataaattgaattgcacataataataattttttccc 942
Db 62 www. ....
Qy 943 aaaaaagtagactgtctatctataaaatttgatcccaatagacaataattcctaaa 1002
Db 122 www. ....
Qy 1003 atgaacaaacatttgaaattctcgatagaaacatttactatttttgattgggacat 1062
Db 182 www. ....
Qy 1063 attcaaaagttattccaaacgttaactttgaaggaaagttgattgagattacacccata 1122
Db 242 www. ....
Qy 1123 tttttgttttcattgaatttcattgaaataataataataataataatgatgatgag 1182
Db 302 www. ....
Qy 1183 attaaacaaagtttattgattgattgatttatttatttatttatttatttatttataa 1242
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Db 542 www. ....
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Db 662 www. ....
Qy 1543 tgataattatgaaaaataataaatttaattataataattcatttcattcattcgtaca 1602
Db 722 www. ....
Qy 1603 a 1603
Db 782 w 782

RESULT 9
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XX
XX AC AAF58257;
XX
XX 24-APR-2001 (first entry)
XX
XX Oligonucleotide D1954.
XX
XX Electron-transfer group; ETM; mismatch; genotyping;
XX gene expression; ss.
XX
XX Synthetic.
XX
XX WO200107665-A2.
XX
XX 01-FEB-2001.
XX
XX 26-JUL-2000; 2000WO-US20476.
XX
XX 26-JUL-1999; 99US-0145695.
XX
XX 17-MAR-2000; 2000US-0190259.
XX
XX (CLIN-) CLINICAL MICRO SENSORS INC.
XX
XX Umek RM;
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XX WPI; 2001-159728/16.
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XX Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface
XX
XX Example 6; Page 127; 159pp; English.
XX
XX The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX
XX Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;
SQ

Query Match 16.0%; Score 278.2; DB 22; Length 936;
Best Local Similarity 0.9%; Pred. No. 4.3e-29;
Matches 7; Conservative 613; Mismatches 161; Indels 0; Gaps 0;

Qy 823 aatttttcttcgaattgtctctacataataataataataatttttaccacttcgt 882
Db 2 www. ....
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Db
190 gagctggatccactagtaacggccgagtgctgctaattcggttg 238

Search completed: April 2, 2002; 09:22:39
Job time: 10390 sec

04-DEC-1998; 98WO-US25832.
17-MAR-1998; 98US-0042780.
04-DEC-1997; 97US-0985090.
(MILL-) MILLENNIUM PHARM INC.
Distefano P., Glucksmann MA, Goodearl ADJ, Xie M;
WPI; 1999-394858/33.
P-PSDB; AAY06323.

New nucleic acid encoding an isolated G-protein coupled receptor
useful for treating nervous system related disorders

Claim 7b; Fig 2; 140pp; English.

This nucleotide sequence, the coding region of which is claimed,
codes for a novel rat G protein coupled receptor, termed
flh84g5 (see AAY06323). The flh84g5 cDNA was isolated from a rat
frontal cortex cDNA library, and has been used to isolate human
flh84g5 (see AAX59167). The invention provides human, rat and mouse
flh84g5 polynucleotides (including polynucleotides encoding the
transmembrane regions of flh84g5 and antisense nucleic acid
molecules), expression vectors, host cells, transgenic animals,
flh84g5 polypeptides and antibodies, and a method of modulating
phosphatidylinositol metabolism. The flh84g5 polypeptides can
(i) interact with a flh84g5 ligand, such as acetylcholine or
carnitine, (ii) interact with a G protein or another protein which
naturally binds to flh84g5, (iii) modulate the activity of an ion
channel (e.g. a calcium activated chloride channel or a potassium
or calcium channel), (iv) modulate cytosolic ion, e.g. calcium
concentration, (v) modulate the release of a neurotransmitter, e.g.
acetylcholine or carnitine from a neuron, (vi) modulate a flh84g5
ligand response in a responsive cell, (vii) signal ligand binding
via phosphatidylinositol turnover, and (viii) modulate phospholipase
C activity. The products can be used to treat: disorders mediated
by abnormal flh84g5 polypeptide activity such as nervous system
related disorders, e.g. amnesia, apraxia, agnosia, amnesiac
dysnomia, amnesiac spatial disorientation, Klüver-Bucy syndrome,
Alzheimer's related memory loss and learning disability; disorders
affecting consciousness such as visual hallucinations, perceptual
disturbances or delirium associated with Lewy body dementia,
schizophrenia, schizophrenia with mood swings,
depressive illness (primary and secondary); affective disorders
such as REM sleep abnormalities in patients suffering from e.g.
depression, paradoxical sleep abnormalities, sleep-wakefulness, and
body temperature or respiratory depression abnormalities during
sleep; disorders affecting pain generation mechanisms e.g. pain
related to irritable bowel syndrome or chest pain; movement
disorders e.g. Parkinson's disease related movement disorders;
eating disorders e.g. insulin hyperscretion related obesity or
drinking disorders, e.g. insular polydipsia; smooth muscle related
disorders, e.g. irritable bowel syndrome, diverticular disease,
urinary incontinence, oesophageal achalasia or chronic obstructive
airways disease; cardiac muscle disorders, e.g. pathologic
bradycardia or tachycardia, arrhythmia, flutter or fibrillation;
and gland related disorder such as xerostomia or diabetes mellitus.
The products can also be used for detection, diagnosis and drug
screening.

Sequence 3244 BP; 609 A; 1052 C; 903 G; 680 T; 0 other;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.6e-07;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps

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Db 130 agcggtgaacaatttcacagagaacagtgtgacctgattaccgcagcttgacc 189

Y 61 ggcctgggtaccactagtaacgccgcagctgtgctggaaattcgcttg 109

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 2, 2002, 05:37:48 ; Search time 1546.5 Seconds
(without alignments)
12055.561 Million cell updates/sec

Title: US-09-811-093-42

Perfect score: 1735

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Scoring table: IDENTITY_NUC

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Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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8: em_estov:**
9: em_hic:**
10: gb_est1:**
11: gb_est2:**
12: gb_hic:**
13: gb_gss:**
14: em_gss_fun:**
15: em_gss_hum:**
16: em_gss_inv:**
17: em_gss_pln:**
18: em_gss_pro:**
19: em_gss_rod:**
20: em_gss_vrt:**
21: em_gss_other:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	131.4	7.6	1101	13	CNS00EVL
c 2	124.2	7.2	1101	13	AL061936 Drosophila
c 3	119.2	6.9	1201	13	CNS0167M
c 4	118.2	6.8	1101	13	CNS00EVL
c 5	117.2	6.8	625	13	CNS036A2
c 6	115.8	6.7	1101	13	CNS0021J
c 7	115.2	6.6	1225	13	CNS0161D
c 8	114	6.6	942	13	CNS00601
c 9	114	6.6	951	13	AZ676519
c 10	113	6.5	1151	11	CG309087
c 11	110	6.3	485	11	CG673765
c 12	110	6.3	638	11	BF294063

c 13	110	6.3	1101	13	CNS00B07
c 14	109	6.3	1092	13	CNS020K7
c 15	108	6.2	430	13	AQ934864
c 16	108	6.2	440	11	BG673763
c 17	108	6.2	466	10	AJ293456
c 18	107.8	6.2	1101	13	CNS00B01
c 19	107	6.2	288	11	BG319604
c 20	106.8	6.2	920	13	AZ691914
c 21	104.8	6.0	437	10	AW697868
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c 24	104.2	6.0	1400	5	BF627293
c 25	103.8	6.0	458	10	AL514085
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c 31	102.8	5.9	1027	13	CNS02450
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c 34	102	5.9	869	13	AF307807
c 35	101.8	5.9	1151	11	BG309087
c 36	101.8	5.9	1169	13	CNS06KHQ
c 37	101.4	5.8	335	10	AL513597
c 38	101.4	5.8	1101	13	CNS001FB
c 39	101.4	5.8	1101	13	CNS0039G
c 40	101.2	5.8	404	10	AL514087
c 41	101.2	5.8	1101	13	CNS00RAE
c 42	101	5.8	1092	13	CNS020K7
c 43	100.8	5.8	356	10	AJ278589
c 44	100.4	5.8	1013	13	CNS06RPQ
c 45	100.2	5.8	693	10	AV682300

ALIGNMENTS

RESULT: 1
CNS00EVL/c
LOCUS

DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC:

BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit fly) genomic survey sequence.

ACCESSION
AL069706.1 GI:4949849

VERSION
GSS.

KEYWORDS
fruit fly.

SOURCE
ORGANISM

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

Direct Submission

TITLE

JOURNAL

COMMENT

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr

Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs for further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammos in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

ECORI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

AL069440 Drosophila
AL175696 Tetraodon
AQ934864 156_A_09-
BG673763 9010_c111
AJ293456 AJ293456
AL057419 Drosophila
BG319604 4dh42 Hum
AZ691914 ENTWU26TR
AW697868 EST0051_C
AL069440 Drosophila
AL053009 Drosophila
BF627293 HVSME000
AL514085 AL514085
AL063921 Drosophila
BE439760 HTM1-619F
AL103436 Drosophila
AL032474 EST01321
AW682474 EST00805
AL212733 Tetraodon
AL514791 AL514791
AL565457 AL565457
AF307807 AF307807
BG309087 HVSMEC000
AL402900 T3 end of
AL513597 AL513597
AL060732 Drosophila
AL063921 Drosophila
AL514087 AL514087
AL077628 Drosophila
AL175696 Tetraodon
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AL412260 T7 end of
AV682300 AV682300

FEATURES	Location/Qualifiers		REFERENCE		Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.	
	source	1..1101	AUTHORS	1 (bases 1 to 1101)	Genoscope	
		/organism="Drosophila melanogaster"	TITLE	Direct Submission		
		/db_xref="taxon:7227"	JOURNAL	Submitted (02-JUN-1999)	Genoscope - Centre National de Sequençage :	
		/clone_lib="RPCI-98"		BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr		
		/note="end : 77"		- Web : www.genoscope.cns.fr)		
BASE COUNT		419 a 91 c 60 g 299 t 232 others	COMMENT		Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammos in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.	
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					/clone_lib="RPCI-98"	
					/note="end : TET3"	
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ORIGIN						
			Query Match		7.2%; Score 124.2; DB 13; Length 1101;	
			Best Local Similarity		43.0%; Pred. No. 1.1e-05;	
			Matches 373; Conservative 47; Mismatches 442; Indels 5; Gaps 2;			
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DB	910	TTAAACACATATTTAAATSTATTATTAATTTTAAATAAANAATTAATTA	851			
QY	855	tataataataattttaccaccttcgttatatttcgaaagaccccttaataat	914			
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DB	730	ATTAATTTTAAAWAAAAAATAAATAAATAAATAAATAAATAAATAAATAA	673			
QY	1035	aacattactattttgaattgggacataattccaaagttttattccaaacgtta	1094			
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QY	1095	ggaaaagttgattgagattacatccattttgttttcattgaaatttcattg	1154			
DB	612	TAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	553			
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DB	495	TT	436			
QY	1275	tcgttgctatttgtagataaatttgtaattttgttatatttaataaattttgat	1334			
DB	435	TT	376			

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 Db 375 TTTTtt 316
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 Qy 1515 aaaatatgggtctcttattcaccttcacattatgataataataaaaataaaattttta 1574
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 Qy 1575 tatataactttctcatcgtacacgctagatatttactatatacaacacttttgt 1634
 Db 135 TTTTtdnttt 76
 Qy 1635 ataaaaaggcgaataagcatta 1661
 Db 75 AAATAAAAAANAANAANAABAA 49

RESULT 3

CNS0167M 1201 bp DNA GSS 26-JUL-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC
 DEFINITION BACN15M24 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL106396
 VERSION AL106396.1 GI:5621701
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Plasmid Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1201)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
 COMMENT - Web : www.genoscope.cns.fr
 Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES

Location/Qualifiers
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 /organism="Drosophila melanogaster"
 /plasmid="pBelOBAC11"
 /db_xref="taxon:7227"
 /clone.lib="DrosBAC"
 /clone="BACN15M24"
 /note="end : 77"
 BASE COUNT 323 a 87 c 79 g 551 t 161 others
 ORIGIN

Query Match 6.9%; Score 119.2; DB 13; Length 1201;
 Best Local Similarity 39.4%; Pred. No. 3.9e-05;
 Matches 349; Conservative 102; Mismatches 428; Indels 6; Gaps 3;
 Qy 584 ttaaaaaaacgttagtcaactcaaacattgtataaccataaacatttaaacgatagattg 643
 Db 317 TTTAATTATGATATAAATTTTCGATAWAATTTWAGWAATAATTTTWAGACGACGATAG 376

Qy 644 aaataaataacgttagatttggtatcccaatttaataatgacaaaatcttaaacgatcgt 703
 Db 377 CAAMGAAATGAATCAAGTGAACCAACCAAAATCTTACCACCTCCAAAGCAAGAAAGCT 436
 Qy 704 atacca----aacttaaacgatcgkatakcaaaatctaaatgatcatgtaccaaaatatt 759
 Db 437 AAAAMGAAACATTTTAARAAAAARTGTTCACTGAAGAAAGAAATGAATGAAGAAACCTT 496
 Qy 760 atgcacattgttggcagggtgggtgacggaaacattttgtatattttctattatgggttg 819
 Db 497 AAGAGGCTTCTCTTTTGAMMTTYYTMMCAHHTTYYCTTSTTTTGGCCAAATCAAAWTKIV 556
 Qy 820 tagaatt 879
 Db 557 TCGCCAGCGTGWATYKMMVCHTSTWNNHHTTTHMMHMMWATAGATTTTATTATTK 616
 Qy 880 cgttatttttcgaagaagccccccttaataaattgaattcgcataataataaaattttt 939
 Db 617 TKTTTtkttt 676
 Qy 940 cccaaaaaagtagactatgtctatctaaattttgattttcccaatataagaacaaattcc 999
 Db 677 TKKTGTDAAAAAAATNTTTTtttttttttttttttttttttttttttttttttttttt 736
 Qy 1000 aaaaagaacaaacatttgaaattctcgatagaaaacatttactttattttgaattggga 1059
 Db 737 GTTTTATGNATTAATTTATATTAAWATTTTWTWTTTW-TTTTTTATTNNAAAA 795
 Qy 1060 catattccaaagtatttccaaacgttaactttgaaggaaagtgtgagattacatcc 1119
 Db 796 ARAATTAATTTTtt 855
 Qy 1120 atattttgttt 1179
 Db 856 TTTTtt 915
 Qy 1180 gagattaaacaaagtatttctgatttgaattcttttttttttttttttttttttttttt 1239
 Db 916 TTTATATATAAAAAAATTTTATATTTTtttttttttttttttttttttttttttttttt 975
 Qy 1240 aaactgtttgcataagacaaatagtttaaccatcggtgtctatctgtagataaattgt 1299
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 Qy 1359 acaaaattgaatttaaaatt 1418
 Db 1096 TTTATTTAATATWMTTWTWTTTATATATATWTTTATTTTtttttttttttttttttt 1155
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 Db 1156 ATATTWTTTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATTATT 1200

RESULT 4

CNS00EVL 1101 bp DNA GSS 04-JUN-1999
 LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC:
 DEFINITION BACR29B23 of RPCR-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
 ACCESSION AL069706
 VERSION AL069706.1 GI:4949849
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 AUTHORS Genoscope.

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Db	1067	ATATATTAATATAWAAAAAATAAATAWAA	1101
RESULT	5		
CNS036A2/c			
LOCUS		625 bp	DNA
DEFINITION		Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 215D15 of library G from Tetraodon nigroviridis, genomic survey sequence.	
ACCESSION		AL229763	
VERSION		AL229763.1	GI:7888758
KEYWORDS		GSS; genome survey sequence.	
SOURCE		Tetraodon nigroviridis.	
ORGANISM		Tetraodon nigroviridis.	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.	

REFERENCE	Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodon.
AUTHORS	1 (bases 1 to 625) Roest-Crollius,H., Jalllon,O., Dasilva,C., Fizames,C., Fisher,C., Bouneau,L., Billaut,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
TITLE	Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 625)
AUTHORS	Roest-Crollius,H., Jalllon,O., Dasilva,C., Bouneau,L., Fisher,C., Barnot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
TITLE	Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL	Unpublished
REFERENCE	3 (bases 1 to 625)
AUTHORS	Genoscope.
TITLE	Direct Submission
JOURNAL	Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
COMMENT	This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/tetraodon .
FEATURES	Location/Qualifiers
source	1..525

[illegible]

Qy 61 gagctcggtaccactagtagtaacggccagtgctgctgaattcggctt 108
Db 334 GAGCTCGGATCCACTAGTAGACGGCCGCCAGTGTGCTGGAATTCGGCTT 287

Search completed: April 2, 2002, 07:01:09
Job time: 5001 sec

INTERFERENCE ONLY

GenCore version 4.5
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OM nucleic - nucleic search, using sw model
Run on: April 2, 2002, 05:41:13 ; Search time 91.56 Seconds
(without alignments)
4291.605 Million cell updates/sec

Title: US-09-811-093-42
Perfect score: 1735
Sequence: 1 agcgataacaatttcacac.....taattggaagcttgtagt 1735

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext.1.0

Searched: 351203 seqs, 113238999 residues

Total number of hits satisfying chosen parameters: 702406

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2.6/ptodata/2/lna/6B-COMB.seq: *
5: /cgn2.6/ptodata/2/lna/PCTUS-COMB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	109	6.3	3244	3 US-09-165-543-4	Sequence 4, Appl
2	92.8	5.3	636	4 US-08-998-416-1137	Sequence 1137, Ap
3	89.8	5.2	837	4 US-08-998-416-288	Sequence 288, App
4	89.2	5.1	7218	1 US-08-232-463-14	Sequence 14, Appl
5	87	5.0	19124	2 US-08-487-826B-13	Sequence 13, Appl
6	86.2	5.0	19124	2 US-08-487-826B-13	Sequence 13, Appl
7	84	4.8	615	4 US-08-998-416-186	Sequence 186, App
8	80.8	4.7	1431	4 US-09-316-083-2	Sequence 2, Appl
9	76.2	4.4	5852	1 US-07-867-106-2	Sequence 2, Appl
10	75	4.3	5852	1 US-07-867-106-2	Sequence 2, Appl
11	74	4.3	240	2 US-08-628-417-6	Sequence 6, Appl
12	73.6	4.2	6243	2 US-09-056-075-1	Sequence 1, Appl
13	73.4	4.2	1511	1 US-07-991-867B-8	Sequence 8, Appl
14	73.4	4.2	1511	1 US-08-107-755A-8	Sequence 8, Appl
15	73.4	4.2	1511	2 US-08-544-332-8	Sequence 8, Appl
16	73.2	4.2	658	4 US-08-998-416-595	Sequence 595, App
17	72.6	4.2	2447	2 US-09-014-969-14	Sequence 14, Appl
18	71.8	4.1	854	4 US-08-998-416-534	Sequence 534, App
19	71.4	4.1	3095	6 5231168-1	Patent No. 5231168
20	71.2	4.1	636	4 US-08-998-416-1137	Sequence 1137, Ap
21	70.8	4.1	724	4 US-08-998-416-683	Sequence 683, App
22	70.4	4.1	732	4 US-08-998-416-1036	Sequence 1036, Ap
23	69	4.0	3701	4 US-08-845-258-10	Sequence 10, Appl
24	69	4.0	3701	4 US-08-990-571-10	Sequence 10, Appl
25	69	4.0	3701	4 US-08-723-142A-10	Sequence 10, Appl
26	68.8	4.0	837	4 US-08-998-416-288	Sequence 288, App
27	68.4	3.9	6152	4 US-08-973-462-1	Sequence 1, Appl

c 28	68.2	3.9	665	2	US-08-883-795A-36	Sequence 36, Appl
c 29	67.6	3.9	615	4	US-08-998-416-186	Sequence 186, App
c 30	67.4	3.9	3701	4	US-08-845-258-10	Sequence 10, Appl
c 31	67.4	3.9	3701	4	US-08-990-571-10	Sequence 10, Appl
c 32	67.4	3.9	3701	4	US-08-723-142A-10	Sequence 10, Appl
c 33	67	3.9	4673	1	US-07-638-431-1	Sequence 1, Appl
c 34	67	3.9	4673	5	PCT-US92-00018-1	Sequence 1, Appl
c 35	67	3.9	8920	2	US-08-446-855A-1	Sequence 1, Appl
c 36	67	3.9	8920	4	US-09-150-741-1	Sequence 1, Appl
c 37	66.8	3.9	8920	4	US-08-446-855A-1	Sequence 1, Appl
c 38	66.8	3.9	8920	4	US-09-150-741-1	Sequence 1, Appl
c 39	66.2	3.8	663	4	US-08-998-416-191	Sequence 191, App
c 40	65.8	3.8	2861	1	US-08-299-953-1	Sequence 1, Appl
c 41	65.8	3.8	2861	1	US-08-459-415-1	Sequence 1, Appl
c 42	65.8	3.8	2861	5	PCT-US95-11231-1	Sequence 1, Appl
c 43	65.8	3.8	3881	1	US-08-299-953-2	Sequence 2, Appl
c 44	65.8	3.8	3881	1	US-08-459-415-2	Sequence 2, Appl
c 45	65.8	3.8	3881	5	PCT-US95-11231-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-165-543-4
; Sequence 4, Application US/09165543
; Patent No. 6093545
; GENERAL INFORMATION:
; APPLICANT: Andrew D.J. Goodearl and Sandra Glucksmann
; TITLE OF INVENTION: Muscarinic Receptors and Uses Therefor
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109

COMPUTER READABLE FORM: disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/165,543
APPLICATION NUMBER: US/09/165,543
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/042,780
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth A. Hanley
REGISTRATION NUMBER: 33,505
REFERENCE/DOCKET NUMBER: MNI-032CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)742-4214
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 3244 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 778..2112
US-09-165-543-4

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Best Local Similarity 100.0%; Pred. No. 4.4e-10;
Matches 109; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-08-487-826B-13/c
: Sequence 13, Application US/08487826B

RESULT 4
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:

Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B.
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NH121.001Cp1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 5.0%; Score 87; DB 2; Length 19124;
Best Local Similarity 46.9%; Pred. No. 1.7e-06;
Matches 438; Conservative 0; Mismatches 485; Indels 10; Gaps 5;
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QY 853 aataataataatatttaccattctgttatatttccgaagacccttaataaat 912
DB 7097 tctatatatatatatatatatttatttctgctacttatataatttacaatatatg 7038
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DB 7037 ---atggttaaaaaataataatttataatgatatataataataatttatttattt 6981
QY 973 ttgattcccatatagacaattctcaaatgacaacatttgaatttcgatatag 1032
DB 6980 ttttaaaaaataatatatatataatttataataatttataataatttataacaaa 6921
QY 1033 aaaaatttactatttgaattgggacatatctcaaaagtatttccaaagtaacttg 1092
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QY 1153 aattaaatgcacacaaaatgatgtatgatgattaaac-caaagtttctcggttattgaatt 1211
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DB 6503 TATATAATAATATATATAGCATCAAAAAAATAAATGATAAATAACAGGAAAAATATA 6444
QY 1511 ctataaaatatgggtctctttttatcaccttccatgataattatgaaaaataaaatt 1570
DB 6443 TTATTATATTATATATATATATATAAATAAATGTTTATCATTTGTTTGTGTTAT 6384
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DB 6323 AAGTAAAAATACACATTATATAATATATATTTCAAAATGAGTTTATAAATAAATGTTCA 6264
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DB 6263 TGTTCTATATATTTTATATAAATGAAAAATATTG 6231

RESULT 6
US-08-487-826B-13
Sequence 13, Application US/08487826B
Patent No. 5993827
GENERAL INFORMATION:
APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellens, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe Martens Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: California
COUNTRY: US
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,826B
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:

NAME: Israelson, Ned
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH121-001CP1
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-826B-13

Query Match 5.0%; Score 86.2; DB 2; Length 19124;
Best Local Similarity 45.2%; Pred. No. 2.2e-06;
Matches 519; Conservative 1; Mismatches 614; Indels 15; Gaps 5;

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QY 637 agaatgaaatacaaatcggttagatttggtctccaaatttaaataaccaaactctaaa 696
DB 4972 AGACAAAATGGNAACATAAANAATGTTACTGTATAGGTAAANAATATATATATAA 5031
QY 697 cgatcgatatccaataacaaacgcakcatcaccaaatcotaatgatcatgtaccaaatat 756
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DB 5092 ATAAATAATTAACATACATTACAPAAATGAATTTCCGATTTTTGTTGTTTGATGAATAT 5151
QY 816 ttgtagaattttctcatttcgaattgttctctacatacaataataataatctttacc 875
DB 5152 TAGGCATTAATTTATATGTGTAATCGGTCTCTATATTAATAATAATAATTTATTTTAA 5211
QY 876 acttcgttatatttcgaaagagccccttaataaattgaattcgcataataataaatt 935
DB 5212 AATGAAATAAATAAATAATCCTGATTTGTAGTTCCAATAGCTTAATAATATAT 5271
QY 936 tttccccaaaaagttagactatgctctatcctcaaaattgtatcccaatatagaacaaat 995
DB 5272 GGACTCATATATATATATATATCTTTTACAAAGAATTAAGTAAATATATTTTAAAT 5331
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DB 5332 CTTAATAAGGAAATAAATAAATAAATAAGATACTGAATAAATAGTCATATATATACA 5391
QY 1056 gggacataticccaagtttatccaaacgtaactttgaaggaaagtgtgagattacc 1115
DB 5392 TTTTAAAAAATGPAACATAAT-PACAAATACGTAAACATGATTATAGAAATAAAGAA 5450
QY 1116 atccatatattttgttttcattgaaattctatcggaataattaaatgcacacaaatgat 1175
DB 5451 TTTAAATTAAGGATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 5510
QY 1176 gtatgagattaaacaaagtttacgttattgaattcttttatttaaaacaaacaaat 1235
DB 5511 ATATATATATATATACATGATTAGTTTGTGAAAAAATTTTAAATATATATATATAT 5570
QY 1236 tttaaaactgtttgcataagaccaaataagttaatccatogtgctctattgtagataaa 1295
DB 5571 AATAAA-----TTAGTTAAATAATAGTATTTTCAACAAATACTAACCTTATAAGTATA 5624
QY 1296 ttgtaatatattttgtataataataatattttgtatttttttttttttttttttttt 1355
DB 5625 TCATATAATATATATATATATATTTTATTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 5684

Query Match 4.7%; Score 80.8; DB 4; Length 1431;
Best Local Similarity 44.4%; Pred. No. 1.5e-05;
Matches 457; Conservative 1; Mismatches 563; Indels 9

Qy	574	acaaaagatttaaaaaaacgtgttagtgcgaatcctaaacaattgtataacccaataaac	633
Db	1125	AGAAATAGATAAATCAAAAGATCTTGAAATTAATAAATAATTAATCTTTACGTGTTTCAAC	1066
Qy	634	gatagaattgaaataaataaatacggttagattggctatccaaaatttaaatgaccaaatct	693
Db	1065	TTGTGAATAACATAACTAGGCTCATATTTTAAATAATATGTATCTTTTAGGATTATA	1006
Qy	694	aaacgctgctatccaaaactaaacgctgcgkacaccaaactcaaatgatcatgtaccaaa	753
Db	1005	CATAGATGATAAAAGAACCATCTGCAGCTGTAAACCCAGCTAACCAATTAATTAATTT	946
Qy	754	tatatatgcacattgttgccgggggttgtagcggaacatttctgtatatattctctattg	813
Db	945	AATATCCATAATATTTTAATAGTAATTTATTAATTAATTAATTAATTAATTAATTAAGG	886
Qy	814	ggtttgtagaatttttccatttttcgaaaattgtctatacaataataaatataaatatttta	873
Db	885	GATATGATTAATTAATTTGATTAATTTATTAATCACTATATTAATTTATTAATAATTAAGT	826
Qy	874	ccacttcgttatatttcgaaaagacccttaataaattgaaattcgcat---ataatt	929
Db	825	AAAAATCTTTCTT?AGCTAAATAGTTTATATATATAGAGAAGCATTAACAAATA	766
Qy	930	aaattttttcccaaaaaagtagactatgtctatctcaaaaatttgatcccaatataga	989
Db	765	AGGATTATCTTTTAAAGTATCCATCCATTTTTCTACTAAAACTATATTTTAAATCTTTT	706
Qy	990	acaaattctcaaatgaacaaacatttgaattctcgatatagaaaacatttactattt	1049
Db	705	ATTAATAAGATAGTATTTAATACATCAPTAGCATGATTAGTAATTTGTAATACCTCCAGG	646
Qy	1050	tgaattgggacatattccaaagtttattcc--aaacgtaacctttgaaggaaaagtgtat	1107
Db	645	ACCNATAACCATCACTTCATTTACCTCGTAATAATCAATCAATAAATTCATTTATTT	586
Qy	1108	gagattacatccatattttgttttcatattgaatttcattcgaaaattaaatgcacac	1167
Db	585	TAAATCTAATACGTGTTTAAATATTTAACTTTTACCTTTATTAATTAATTTTAAACATATA	526
Qy	1168	aaatgatgatgagattaaaccaaagttatcgttattgaattcttttataaaaaacc	1227
Db	525	ATTATTAGGAATCATATTTAAACATATCTAAATATTTCATATATTTATTAATTAATAATTT	466
Qy	1228	aacaaaatttttaaaactgttgcgaatgagaccaaataagttaaacccatcggtctattg	1287
Db	465	ATCCATTAATAAATAATTAATAGATA--AATTAGTTTCAATATATAGAAAGTTTATAAAT	409
Qy	1288	tagataaattgtaattttgttatatttaataaatattttgattttatttggatcatattt	1347
Db	408	TAAATTTATTCATTAATATTTTAAATAATTCATATATATTTTAAATGAATATTTATTTATTT	349
Qy	1348	gtatttagataacaaaattaaagattaaatatattttatatcttaataataaacatttgt	1407
Db	348	ATTAATTAATTAATTCATTTCCATTTTCATTTTATTTTAAATATAAATAAAGTATATAA	289
Qy	1408	taattttttctatttttagaccattctcttatttttatataaacatttttaataacataaagt	1467
Db	288	TAAATTTAATTCATTAATATTTTGAATTCATTAATCTTTTATTAAGACATAGGTGTACG	229

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RESULT      8
US-09-316-083-2/c
; Sequence 2, Application US/09316083A
; Patent No. 6280942
; GENERAL INFORMATION:
; APPLICANT: The Institute of Physical and Chemical Research
; TITLE OF INVENTION: Endonuclease
; FILE REFERENCE: PH-651
; CURRENT APPLICATION NUMBER: US/09/316.083A
; CURRENT FILING DATE: 1999-05-20
; EARLIER APPLICATION NUMBER: JP98/141861
; EARLIER FILING DATE: 1998-05-22
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0

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RESULT 11
US-08-628-417-6/c
; Sequence 6, Application US/08628417
; Patent No. 5627054
; GENERAL INFORMATION:
; APPLICANT: GILLESPIE, DAVID
; TITLE OF INVENTION: COMPETITOR PRIMER ASYMMETRIC
; TITLE OF INVENTION: POLYMERASE CHAIN REACTION
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL
; ADDRESS: DEFENSE COMMAND
; STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC)
; CITY: ABERDEEN PROVING GROUND
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/628.417
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: RIFTONI, ULYSSES J
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 398-94
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158

Query Match 4.3%; Score 75; DB 1; Length 5852;
Best Local Similarity 44.9%; Pred. NO. 0.00014;
Matches 372; Conservative 0; Mismatches 450; Indels 7; Gaps 2;

REFERENCE/DOCKET NUMBER: UFI14.C3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1511 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Amsacta moorei entemopoxvirus

FEATURE:

NAME/KEY: CDS

LOCATION: complement (18..218)

FEATURE:

NAME/KEY: CDS

LOCATION: complement (234..782)

FEATURE:

NAME/KEY: CDS

LOCATION: 852..1511

US-07-991-867B-8

Query Match 4.2%; Score 73.4; DB 1; Length 1511;

Best Local Similarity 46.3%; Pred. No. 0.00024;

Matches 355; Conservative 0; Mismatches 401; Indels 11; Gaps 3;

QY 824 attttttcatttcgaaattgttctatacaataataataataattttaccacttcgtt 883
 DB 421 ATATTCTGTAAAGTCACAAATTTATCCAGCACAATACATTTTTTTTATTATTAGCC 480
 QY 884 atatttcgaagaagcccttaataaattgaattcgcatataataattttttccca 943
 DB 481 ATTTATCACAAATGTTCTAAATCATTTCTCAAAAAATGACACTCATCTATGCCA 540
 QY 944 aaaaaagtagactatgtctatcaaaaaattgattcccaataatagacaaaattctcaaaa 1003
 DB 541 ATAAATCATCAAT-----TATTCAGCATATTGATTTTCATTAATTAATTTTGTGTTAA 595
 QY 1004 tgaacaaacatttgaattctcgatagaaacatttctatttgaattgggacata 1063
 DB 596 TGTATAAATATTCTTTATTATATATATTTCCGTCATGATTTATATATTTTATTATATA 655
 QY 1064 ttccaaagtatttccaaacgtaactttgaaggaagaattgattgagattacatccatat 1123
 DB 656 ATCTATTATCTATATATGAGTTATTAATTAACACATTTTGTGATTAGATAAATATATCTAT 715
 QY 1124 ttttgttttcattgaatttcattcgatggaaaaataaaatgacacaaaatgatgata 1183
 DB 716 TAAATTTTCGCAATCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 775
 QY 1184 ttaacacaaagtatttcgattgatttcttttataaaacacacaaaatttttaaac 1243
 DB 776 -TCGACATTTTATTATTATTGATATATTTTTCAAAAAATAATTAATCAATGAAAAA 834
 QY 1244 tttgttgaatgacaaatagattgtaacttcgctggtctattgtagataaattgtaata 1303
 DB 835 AAAATAAATAATTAACAAATGGATTACTAAATTCGATATAATTTTAAATAATTTTAA 894
 QY 1304 tttgttattataataaattttgatttttttttttttttttttttttttttttttttttt 1363
 DB 895 ATATATTAATTTAAAAAATAAATAAATTAACAGAGATGTTTATTAATTAATTAATATAT 954
 QY 1364 attagatttaataatt 1423
 DB 955 TAAAAAATTAAGTTAGAGATTGCAATATATATATATATATATATATATATATATATAT 1014
 QY 1424 agaccatttcttt 1483
 DB 1015 ATAATATATCCAGAAA-----ATATTAAAAAGTTATATATATTTTCAATTTTAAATTTATTA 1069

QY 1484 tattattttttatccaaagaaaaaataatgctataaaatatgggtcttttttttttttttt 1543
 DB 1070 TTTAAATTTTATAACAAAATTAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1129
 QY 1544 gataaattatgaaaaataaaataaaatttaattataataattcatttca 1590
 DB 1130 TAGCAATATAAGTAAT 1176

RESULT 14

US-08-107-755A-8

Sequence 8, Application US/08107755A

Patent No. 5721352

GENERAL INFORMATION:

APPLICANT: Moyer, Richard W.

APPLICANT: Hall, Richard L.

APPLICANT: Gruidl, Michael E.

TITLE OF INVENTION: No. 5721352el Entomopoxvirus Expression System

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: David R. Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: Florida

COUNTRY: U.S.A.

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,755A

FILING DATE: 19-AUG-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/827,658

FILING DATE: 30-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/657,584

FILING DATE: 19-FEB-1991

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UFI14.C2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (904) 375-8100

TELEFAX: (904) 372-5800

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 1511 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Amsacta moorei entemopoxvirus

FEATURE:

NAME/KEY: CDS

LOCATION: complement (18..218)

FEATURE:

NAME/KEY: CDS

LOCATION: complement (234..782)

FEATURE:

NAME/KEY: CDS

LOCATION: 852..1511

US-08-107-755A-8

Query Match

Best Local Similarity 4.2%; Score 73.4; DB 1; Length 1511;

Matches 355; Conservative 0; Mismatches 401; Indels 11; Gaps 3;

